

0400 04-12-01

#3

OIKE

RAW SEQUENCE LISTING

DATE: 04/04/2001

PATENT APPLICATION: US/09/809,745

TIME: 14:20:45

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\04042001\I809745.raw

4 <110> APPLICANT: Weiner, Howard L.
 5 Maron, Ruth
 6 Libby, Peter
 8 <120> TITLE OF INVENTION: SUPPRESSION OF VASCULAR DISORDERS BY
 9 MUCOSAL ADMINISTRATION OF HEAT SHOCK PROTEIN PEPTIDES
 12 <130> FILE REFERENCE: B0801/7202 (AWS)
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/809,745
 C--> 14 <141> CURRENT FILING DATE: 2001-03-15
 14 <150> PRIOR APPLICATION NUMBER: US 60/189,855
 15 <151> PRIOR FILING DATE: 2000-03-15
 17 <160> NUMBER OF SEQ ID NOS: 3
 19 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 540
 23 <212> TYPE: PRT
 24 <213> ORGANISM: M. tuberculosis
 26 <400> SEQUENCE: 1
 27 Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu
 28 1 5 10 15
 29 Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro
 30 20 25 30
 31 Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile
 32 35 40 45
 33 Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro
 34 50 55 60
 35 Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr
 36 65 70 75 80
 37 Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln
 38 85 90 95
 39 Ala Leu Val Arg Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
 40 100 105 110
 41 Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Glu Lys Val Thr Glu
 42 115 120 125
 43 Thr Leu Leu Lys Gly Ala Lys Glu Val Glu Thr Lys Glu Gln Ile Ala
 44 130 135 140
 45 Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile
 46 145 150 155 160
 47 Ala Glu Ala Met Asp Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu
 48 165 170 175
 49 Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg
 50 180 185 190
 51 Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Pro Glu Arg
 52 195 200 205
 53 Gln Glu Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys
 54 210 215 220
 55 Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gly
 56 225 230 235 240

ENTERED

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57 Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala
58                               245                               250                               255
59 Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val
60                               260                               265                               270
61 Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln
62                               275                               280                               285
63 Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Val Gly
64                               290                               295                               300
65 Leu Thr Leu Glu Asn Ala Asp Leu Ser Leu Leu Gly Lys Ala Arg Lys
66                               305                               310                               315                               320
67 Val Val Val Thr Lys Asp Glu Thr Thr Ile Val Glu Gly Ala Gly Asp
68                               325                               330                               335
69 Thr Asp Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Gln Glu Ile Glu
70                               340                               345                               350
71 Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala
72                               355                               360                               365
73 Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu
74                               370                               375                               380
75 Val Glu Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asn
76                               385                               390                               395                               400
77 Ala Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Val Thr
78                               405                               410                               415
79 Leu Leu Gln Ala Ala Pro Thr Leu Asp Glu Leu Lys Leu Glu Gly Asp
80                               420                               425                               430
81 Glu Ala Thr Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu
82                               435                               440                               445
83 Lys Gln Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu
84                               450                               455                               460
85 Lys Val Arg Asn Leu Pro Ala Gly His Gly Leu Asn Ala Gln Thr Gly
86                               465                               470                               475                               480
87 Val Tyr Glu Asp Leu Leu Ala Ala Gly Val Ala Asp Pro Val Lys Val
88                               485                               490                               495
89 Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu Phe Leu
90                               500                               505                               510
91 Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Glu Lys Ala Ser
92                               515                               520                               525
93 Val Pro Gly Gly Gly Asp Met Gly Gly Met Asp Phe
94                               530                               535                               540
96 <210> SEQ ID NO: 2
97 <211> LENGTH: 573
98 <212> TYPE: PRT
99 <213> ORGANISM: H. sapiens
101 <400> SEQUENCE: 2
102 Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg
103 1 5 10 15
104 Val Leu Ala Pro His Leu Thr Arg Ala Tyr Ala Lys Asp Val Lys Phe
105 20 25 30
106 Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala
107 35 40 45

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```

108 Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile
109      50                      55                      60
110 Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val
111      65                      70                      75                      80
112 Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys
113                      85                      90                      95
114 Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly
115                      100                     105                     110
116 Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe
117                      115                     120                     125
118 Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg Gly Val
119      130                      135                      140
120 Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln Ser Lys
121      145                      150                      155                      160
122 Pro Val Thr Thr Pro Glu Glu Ile Ala Gln Val Ala Thr Ile Ser Ala
123                      165                      170                      175
124 Asn Gly Asp Lys Glu Ile Gly Asn Ile Ile Ser Asp Ala Met Lys Lys
125                      180                      185                      190
126 Val Gly Arg Lys Gly Val Ile Thr Val Lys Asp Gly Lys Thr Leu Asn
127      195                      200                      205
128 Asp Glu Leu Glu Ile Ile Glu Gly Met Lys Phe Asp Arg Gly Tyr Ile
129      210                      215                      220
130 Ser Pro Tyr Phe Ile Asn Thr Ser Lys Gly Gln Lys Cys Glu Phe Gln
131      225                      230                      235                      240
132 Asp Ala Tyr Val Leu Leu Ser Glu Lys Lys Ile Ser Ser Ile Gln Ser
133                      245                      250                      255
134 Ile Val Pro Ala Leu Glu Ile Ala Asn Ala His Arg Lys Pro Leu Val
135                      260                      265                      270
136 Ile Ile Ala Glu Asp Val Asp Gly Glu Ala Leu Ser Thr Leu Val Leu
137      275                      280                      285
138 Asn Arg Leu Lys Val Gly Leu Gln Val Val Ala Val Lys Ala Pro Gly
139      290                      295                      300
140 Phe Gly Asp Asn Arg Lys Asn Gln Leu Lys Asp Met Ala Ile Ala Thr
141      305                      310                      315                      320
142 Gly Gly Ala Val Phe Gly Glu Glu Gly Leu Thr Leu Asn Leu Glu Asp
143                      325                      330                      335
144 Val Gln Pro His Asp Leu Gly Lys Val Gly Glu Val Ile Val Thr Lys
145                      340                      345                      350
146 Asp Asp Ala Met Leu Leu Lys Gly Lys Gly Asp Lys Ala Gln Ile Glu
147      355                      360                      365
148 Lys Arg Ile Gln Glu Ile Ile Glu Gln Leu Asp Val Thr Thr Ser Glu
149      370                      375                      380
150 Tyr Glu Lys Glu Lys Leu Asn Glu Arg Leu Ala Lys Leu Ser Asp Gly
151      385                      390                      395                      400
152 Val Ala Val Leu Lys Val Gly Gly Thr Ser Asp Val Glu Val Asn Glu
153                      405                      410                      415
154 Lys Lys Asp Arg Val Thr Asp Ala Leu Asn Ala Thr Arg Ala Ala Val
155                      420                      425                      430
156 Glu Glu Gly Ile Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile

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```

157          435          440          445
158 Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly
159          450          455          460
160 Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala
161 465          470          475          480
162 Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln
163          485          490          495
164 Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn
165          500          505          510
166 Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala
167          515          520          525
168 Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val
169          530          535          540
170 Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala
171 545          550          555          560
172 Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe
173          565          570
175 <210> SEQ ID NO: 3
176 <211> LENGTH: 544
177 <212> TYPE: PRT
178 <213> ORGANISM: C. pneumoniae
180 <400> SEQUENCE: 3
181 Met Ala Ala Lys Asn Ile Lys Tyr Asn Glu Glu Ala Arg Lys Lys Ile
182 1          5          10          15
183 His Lys Gly Val Lys Thr Leu Ala Glu Ala Val Lys Val Thr Leu Gly
184          20          25          30
185 Pro Lys Gly Arg His Val Val Ile Asp Lys Ser Phe Gly Ser Pro Gln
186          35          40          45
187 Val Thr Lys Asp Gly Val Thr Val Ala Lys Glu Ile Glu Leu Glu Asp
188          50          55          60
189 Lys His Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
190 65          70          75          80
191 Thr Ala Asp Lys Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
192          85          90          95
193 Glu Ala Ile Tyr Ser Glu Gly Leu Arg Asn Val Thr Ala Gly Ala Asn
194          100          105          110
195 Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Lys Val Val Val
196          115          120          125
197 Asp Glu Leu Lys Lys Ile Ser Lys Pro Val Gln His His Lys Glu Ile
198          130          135          140
199 Ala Gln Val Ala Thr Ile Ser Ala Asn Asn Asp Ser Glu Ile Gly Asn
200 145          150          155          160
201 Leu Ile Ala Glu Ala Met Glu Lys Val Gly Lys Asn Gly Ser Ile Thr
202          165          170          175
203 Val Glu Glu Ala Lys Gly Phe Glu Thr Val Leu Asp Val Val Glu Gly
204          180          185          190
205 Met Asn Phe Asn Arg Gly Tyr Leu Ser Ser Tyr Phe Ser Thr Asn Pro
206          195          200          205
207 Glu Thr Gln Glu Cys Val Leu Glu Asp Ala Leu Ile Leu Ile Tyr Asp

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```

208      210      215      220
209 Lys Lys Ile Ser Gly Ile Lys Asp Phe Leu Pro Val Leu Gln Gln Val
210 225      230      235      240
211 Ala Glu Ser Gly Arg Pro Leu Leu Ile Ile Ala Glu Glu Ile Glu Gly
212      245      250      255
213 Glu Ala Leu Ala Thr Leu Val Val Asn Arg Leu Arg Ala Gly Phe Arg
214      260      265      270
215 Val Cys Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met
216      275      280      285
217 Leu Glu Asp Ile Ala Ile Leu Thr Gly Gly Gln Leu Val Ser Glu Glu
218      290      295      300
219 Leu Gly Met Lys Leu Glu Asn Thr Thr Leu Ala Met Leu Gly Lys Ala
220 305      310      315      320
221 Lys Lys Val Ile Val Thr Lys Glu Asp Thr Thr Ile Val Glu Gly Leu
222      325      330      335
223 Gly Asn Lys Pro Asp Ile Gln Ala Arg Cys Asp Asn Ile Lys Lys Gln
224      340      345      350
225 Ile Glu Asp Ser Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg
226      355      360      365
227 Leu Ala Lys Leu Ser Gly Gly Val Ala Val Ile Arg Val Gly Ala Ala
228      370      375      380
229 Thr Glu Ile Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Gln
230 385      390      395      400
231 His Ala Thr Ile Ala Ala Val Glu Glu Gly Ile Leu Pro Gly Gly Gly
232      405      410      415
233 Thr Ala Leu Val Arg Cys Ile Pro Thr Leu Glu Ala Phe Leu Pro Met
234      420      425      430
235 Leu Ala Asn Glu Asp Glu Ala Ile Gly Thr Arg Ile Ile Leu Lys Ala
236      435      440      445
237 Leu Thr Ala Pro Leu Lys Gln Ile Ala Ser Asn Ala Gly Lys Glu Gly
238      450      455      460
239 Ala Ile Ile Cys Gln Gln Val Leu Ala Arg Ser Ala Asn Glu Gly Tyr
240 465      470      475      480
241 Asp Ala Leu Arg Asp Ala Tyr Thr Asp Met Ile Asp Ala Gly Ile Leu
242      485      490      495
243 Asp Pro Thr Lys Val Thr Arg Ser Ala Leu Glu Ser Ala Ala Ser Ile
244      500      505      510
245 Ala Gly Leu Leu Leu Thr Thr Glu Ala Leu Ile Ala Asp Ile Pro Glu
246      515      520      525
247 Glu Lys Ser Ser Ser Ala Pro Ala Met Pro Ser Ala Gly Met Asp Tyr
248      530      535      540

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VERIFICATION SUMMARY

DATE: 04/04/2001

PATENT APPLICATION: US/09/809,745

TIME: 14:20:46

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\04042001\I809745.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date